

FIGURE 1

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGA
 GAGAAGCGCCTGCAGCCAAACCAAGGCTCAGGCTGTGCTCACAGTTTCTCTGGCGGCATGTAA
 AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCCGACGGCCTGAGGATGGACCC
 CAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGA
 AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCT
 CTGTGGAGGCGAGAGCCAGTGGAGCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCTGCA
 ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATG
 TGAGGAGCCGCCCGGAGCCAAGCAGGAGGGGAAGAGGCTTTCATAGATTCTATTACAAAGA
 ATAACCACCATTGTCAGGAGCCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG
 CTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTGAGGGCACTGAGGAGGGCTC
 GCCAAGAGAGTTTCATTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCA
 CCTACACCTTCATTGTGCCCCAGCAGCGGGTACGGGTGCCATCTGCGTCAACTCCAAGGAG
 CCTGAGGTGCTTCTGGAGAACCAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCT
 GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGAGGTGGACGGCGGCATTG
 TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC
 TACATGCAGTCTCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCAGCT
 GGAGAACAGGATCTGAACAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC
 TGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCAACAACCATAGAGATCATCGCGCAG
 CTTGAGGAGCACTGCCAGAGGGTGCCCTCGGGCAGGCCGTCGCCAGCCACCCCGCTGC
 CCCGCCCGGGTCTACCAACCAACCCACCTACAACCGCATCATCAACAGATCTCTACCAACG
 AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCCATATGCCACTCTC
 ACCAGCTCCCATCTTCCACCGACAAGCGTCTGGGCCCATGGAGAGACTGCTGCAAGGCCT
 GGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCGGAGAACACCAACCGCCTCA
 TGCAGGTGTGGTGCAGCACAGAGACACGACCCCGGGGCTGGACCCGTCATCCAGAGACGCGTG
 GATGGCTCTGTTAACTTCTTCAGGAACCTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGA
 CGGCGAATACTGGTGGGCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAC
 TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAGTCTTTGCGAATACGCCAGTTTCCGC
 CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA
 CTCCTTTACATGGCACACCGGCAAGCAGTTTCAACACCTGGACAGAGATCATGATGCTACA
 CAGGAACACTGTGCCACTACCAGAAGGGAGGCTGGTGGTATACGCCCTGTGCCCATCCAAC
 CTCACGGGGTCTGGTACCGGGGGCCATTACCGGAGCCGCTACCAGGACGGTCTACTG
 GGCTGAGTTCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGATCCGACCGAACC
 CCAACACCTTCCACTAAGCCAGCTCCCCCTCTGACCTCTCGTGGCCATTGCCAGGAGCCCA
 CCCTGGTCAGCGTGGCCACAGCACAAAGAACAACCTCTCACCAGTCTATCCTGAGGCTGGGA
 GGACCGGGATGCTGGATTCTGTTTCCGAAGTCACTGCAGCGGATGATGGAACATGAATCGAT
 ACGGTGTTTTCTGTCCCTCACTTTCTTCAACACGACAGCCCTCATGCTCTCCAGGACA
 GGACAGGACTACAGACAACCTTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

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FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRVTGAICVNSKEPEVLLNLRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLR
KESRMNSRVTLQYMQLLHEIIRKRDNALELSQLENRILNQATDMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHCQRPVSARPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMTLTSLPSSTDKPSGFPWRDCLQALEDGHDTSIIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFRRNWETKYQGFNGIDGEYWLGLENIYWLTNQGNKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKRLRGYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYHQ
KGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH
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Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.

amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,
465-471, 473-479

Amidation site.

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

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FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCCAGCCGCGTCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGCTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCAGGGCCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT
GTTCCCTCTTTCGGGGGTCTCACCAGAAGAGGTTCTTGGGGGTGCGCCCTCTGAGGAGGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTC
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCCTTCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTGCGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT
GGCAGTAATACGGACTCTTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTtaggacatactcg
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGCTGTCTGTCATCTACTTTGTCTGGAATGTCTAAATGTTTC
TGtagcagaaaaacacgataaagctatgatctttatttagag

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FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846

<subunit 1 of 1, 117 aa, 1 stop

<MW: 12692, pI: 7.50, NX(S/T): 0

MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ

AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDK

Important features:**Signal peptide:**

amino acids 1-16

N-myristoylation sites.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGACCCG
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCTTTGCTGAAGCCCGAGTGGGAGAA
GCCCGGGCAAACGCAGGCTAAGGAGACCAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGG
AGCGCGAGAAATCCAACGCTGCAAGTGTGTACGAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAATAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTATTTTCTGCCTAAACCACTGAAAGTGCCCATGT
ACAAGGAGCCATCACTGCAGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAAC
AAGAGCAGAAGTGCTCTTGGCGTGCTGAACGGAGGCAAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTACCCAAAAGTTCAAATTTGTGAGTACATTTACCAAACAAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLRQKRQAREREKSNACKCVSSPSKGKTS CDKNKLNVFSRVKLF GSKKRRRRRP
 EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
 MNSEGILYTSLEFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLG LNKEGEIMKGNHVK
 KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 7

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGC GCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACA**TAG**

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FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDSPASARRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSITT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

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FIGURE 9

CTCGCAGCCGAGCGCGGCCGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCA
 GACGCCCCCAAGATTGTTGTGAGGAGCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAAGCT
 GTGTCCAGACTGAGGCCCACTTTCGATTGTTTAACATACTTAGAAAATGAAGTGTTTCATTTT
 TAACATTCTCTCTCCAATTGGTTAATGCTGAATTACTGAAGAGGGCTAAGCAAAACAGGTT
 GCTTGGCGTGGAGGCTCTGCAGTGGCTGGGAGGACCCGGCGCTCTCCCGTGTCCTCTCCA
 CGACTCGGCTCGGCCCTCTGGAAATAAAACACCCGCGAGCCCGAGGCCCGAGAGGCGCGA
 CGTGCCCGAGCTCTCTCGGGGGTCCCGCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCTCTCC
 TCGCGCGTCTTGACATGCCAGGAATAAAAGGATACTCACTGTTACCATTTCTGGCTCTCTG
 TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT
 CAGGACAGTGTGTTAGATATTGATGAATGCCGAACCATCCCGAGGCCCTGCCGAGGAGACATG
 ATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCGCCGGACAAACCTGTGTATCGAGG
 GCCCTACTCGAACCCCTACTCGACCCCTACTCAGGTCGGTACCCAGCAGCTGCCCAACAC
 TCTCAGTCCAAACTATCCACAGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCCAGATG
 GATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCAACAGTGCAACCC
 CACCCAGATCTGCATCAATAGTGAAGCGGGTACACCTGCTCTGCACCCGAGGATGTAATGGC
 TTTCTGGAAGGCGAGTGTCTAGACATTGATGAATGTCGCTATGGTTACTGCCGAGCAGTCTGT
 GCGAATGTTCTGGATCTCTATTCTGTACATGCAACCCCTGGTTTTACCCCTCAATGAGGATGG
 AAGGCTCTTGCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAAACCTCGCTCA
 ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAACCTTGAGGAAGATGGCGTT
 CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAA
 CCAGCCCGGACATACTTTCTGCTCCTGCCCTCCAGGCTACATCTGCTGGATGACAACCGAA
 GCTGCCAAGACATCAACGAATGTGAGCACAGGAACACACGTGCAACCTGCAGCAGACGTGC
 TACAATTTACAAGGGGGCTTCAATGCAATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAG
 GATCAGTGATAACCGCTGTATGTGCTCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTA
 CCATCTGTGACCGGACATGGACGTGGTGTCAGGACGCTCCGTTCCCGCTGACATCTTCCAA
 ATGCAAGCCACGACCCGCTACCCCTGGGGCCTATTACATTTCCAGATCAAATCTGGGAATGA
 GGGCAGAGAATTTTACATCGCGGCAAACGGGCCCATCAGTGCCACCTGGTGATGACACGCC
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 AACTTCAGAGCGAGTCCGTGATCCGACTGCGGATATATGTGTGCGAGTACCCATTCTGAGC
 CTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGACAGGAGAGAGAGGAAA
 TAACAGAGAGAATGAGAGCGACACAGACGTTAGGCATTTCCTGCTGAACGTTTCCCGGAA
 GTCAGCCCGACTTCTGACTCTCACCTGTACTATTGCAGACCTGTACCTTGAGGACTTG
 CCACCCCAAGTTCCATGACACAGTTATCAAAAGTATTATCATTTGCTCCCTGATAGAAGA
 TTGTTGGTGAAATTTCAAGGCCTTCAGTTTATTTCCACTATTTCAAAGAAAATAGATTAGG
 TTTGCGGGGCTCTGAGTCTATGTTCAAAGACTGTGAACAGCTTGCTGTCACTTCTTCACCTC
 TTCCACTCTTCTCTCACTGTGTTACTGCTTTGCAAGACCCGCGAGCTGGCGGGGAACCTT
 GGGAGTAGCTAGTTTGCTTTTTGCGTACACAGAGAAGGCTATGTAACAACAACCACAGCAGGA
 TCGAAGGGTTTTAGAGAAATGTGTTTCAAACCATGCCTGGTATTTTCAACCAATAAAGAAAG
 TTTCACTGTCTCTTAAATTTGTATAACGTTTAAATCTGTCTTGTTCATTTGAGTATTTT
 AAAAAATATGTCGTAGAATTTCCTTCGAAGGCCCTTCAGACACATGCTATGTTCTGTCTTCCC
 AAACCGAGTCTCCTCTCCATTTTAGCCCAAGTGTTTTCTTAGGAGCCCTTAATCTTGCTTT
 CTTTAGAATTTTTACCAATTGGATTGGAATGCAGAGGTCTCCAACCTGATTAATATTTGA
 AGAGA

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FIGURE 10

MPGIKRLTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ
NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAAPLSAPNYPTISRPLICRFGYQMDESNO
CVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPG
SYSCTCNPGFTLNE DGRSCQDVNECATENPCVQTCVNTYGS LICRCDPGYELEEDGVHCSDM
DECSFSEFLCQHECVNQPGTYFCSCP PGYIILLDDNRSCQDINECEHRNHTCNLQOTCYNLQG
GFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATT
RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGS
SVIRLRIYVSQYPF

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

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FIGURE 11

CAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
 GACCTCGACCCACGCGTCCGAACACAGGTCCCTGTTGCTGCAGAGAAGCAGTTGTTTTGCTG
 GAAGGAGGGAGTGC GCGGGCTGCCCGGGCTCCTCCCTGCCGCTCCTCTCAGTGGATGGTT
 CCAGGCACCCCTGTCTGGGGCAGGGAGGGCACAGGCCGTGCACATCGAAGGTGGGGTGGGACCA
 GGCTGCCCCCTCGCCCCAGCATCCAAGTCCCTCCCTTGGGCGCCCGTGGCCCTGCAGACTCTCA
 GGGCTAAGGTCCTCTGTTGCTTTTGGTTCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT
 AGCTTGAAGGAGGCACCA**ATG**CAGGAGCTGCATCTGCTCTGGTGGCGCTTCTCCTGGGCGCTG
 GCTCAGCGCTGCCCTGAGCCCTGCGACTGTGGGGAAGAATATGGCTCCAGATCGCCGACTG
 TGCTTACCGCGACCTAGAATCCGTGCCGCTGGCTTCCCGGCCAATGTGACTACACTGAGCC
 TGTGAGCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCAGGGAGGTGCCCTGCTGCAG
 TCGCTGTGGCTGGCACACAATGAGATCCGCAGGTTGGCCGCGGAGCCCTGGCCCTCTCTGAG
 CCATCTCAAGAGCCTGGACCTGAGCCACAATCTCATCTCTGACTTGGCTGGAGCGACCTGC
 ACAACCTCAGTGCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGC
 GACGCCCTCCGCGAGCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGCACAC
 ATTGGCCGAGGGCACCTTCAACCCGCTCACCGCGCTGTCCACCTGCAGATCAACGAGAACC
 CTTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCCTGACCACGGCCGTGCC
 ATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCATGTGCTCAAGGGTACACCGCTGAG
 CCGCTTGC CGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTCAACCAACCGCAGG
 ATGGTGCCGAGCTGCGGCCCTGGTTTGTGCTGGCACTGCACTGTGATGTGGACGGGACGCCG
 GCCCCCTCAGCTTCACTGGCACATCCAGATACCCAGTGGCATTGTGGAGATCACCGACCCCAA
 CGTGGGCACCTGATGGGCGTGCCCTGCCTGGCACCCCTGTGGCCAGCTCCGAGCGCGCTTCC
 AGGCCCTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC
 AGCTGCCTGGCCACCAATGAGCTGGGCAGTGTGAGAGCTCAGTGGACGTGGCACTGGCCAC
 GCCCGGTGAGGGTGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAA
 AGGGCTGCTATACGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATC
 ATCTACCTCAGCCGTGCTGGGAACCCCTGAGGCTGCAGTCGAGAAAGGGGTCCCTGGGCACT
 GCCCCAGGCCGTGCTCCTGCTGGGCCAAAGCCTCCTCCTCTCTCTTCTCTCCTCAGCTCCTCT**CT**
AGCCCCACCCAGGGCTTCCCTAACTCCTCCCTTGGCCCTACCAATGCCCTTTAAGTGCTG
 CAGGGCTTGGGGTTGGCAACTCCTGAGGCCGTGCATGGGTGACTTCACATTTTCCACTCTCT
 CTTTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAACACTAGTGA
 CTAGGATAGAATTTGATCCCTAACTCACTGCTGTGCGGTGCTCATTGCTGCTAACAGCATGTG
 CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCCTAATCCAAC TGGGAGAA
 GCCTCAGTGGTGGAAATTCAGGCACCTGTGACTGTCAAGCTGGCAAGGGCCAGGATTGGGGGA
 ATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAGGAGGATGG
 GAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCTGCT
 CTTTGCTTTTTCTGATGATTTGGGGCTTGGGAGTCCCTTGCTCCTCATCTGAGACTGAAA
 TGTGGGGATCCAGGATGGCCCTTCTTCTCTTACCCTTCTCCTCCTCAGCCTGCAACCTCTAT
 CTTGGAACCTGTCTCTCTTCTCTCCCCAACTATGCATCTGTTGCTGCTCCTCTGCAAAAGGC
 CAGCCAGCTTGGGACGAGCAGAGAAATAAACAGCATTTCTGATGCCAAAAA AAAAAAAAAA
 AAGGGCGGCGGACTCTAGAGTCGACCT

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FIGURE 12

MQELHLLWALLLGLAQACPEPCDCGEKYGFQIADCA YRDLESVPPGF PANVTTL SLSANRL
PGLPEGA FREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSAL
QLLKMSDNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPF DCTC
GIVWLKTWALT TAVSIPEQDNI ACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELR
PGFVLALHCDVDGQPAPQLHWHIQIPSGIVEITS PNVGTDGRALPGTPVASSQPRFQAFANG
SLLI PDFGKLEEGTY SCLATNELGSAESSVDVALATPGE GEDTLGRRFHGKAVEGKGCYTV
DNEVQPSGPE DNVV IYLSRAGNPEAAVAEGVPGQLPPG LLLLQSLLLFFFLT SF

Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites.

amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site.

amino acids 319-326

N-myristoylation sites.

amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,
334-340, 350-356, 394-400

Amidation site.

amino acids 355-359

Leucine rich repeats.

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain.

amino acids 180-230

FIGURE 13

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC
AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGC
AGCGAGGAGGTCTGAGCAGCATGGCCCGGAGGAGCGCCTTCCCTGCCGCCGCTCTGGCT
CTGGAGCATCTCTGTGCTGCTGGCACTGCGGGCGGAGGCCGGGCCGCCGAGGAGGAGA
GCCTGTACCTATGGATCGATGCTACCCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
CTGATTGTTTTAGAGGGGAAAATGGCACCTTTTACACATGATTTAGAAAAGCGCAACAGAG
AATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
CAGAATACTTCTATGAATTCCTGTCTTGGCTCCCTGGATAAAGGCATCATGGCAGATCCA
ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCCTCACAAAGGCATCAGTTGTTCAAGTTGGTTT
CCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT
CTGAAGGCAACACCATTTCTCAAACACCTCAAATGCTATCTTCTTTAAACATGTCAACAA
GCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAGACGCATCTGCGAGTG
TCCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG
GTGGACTTTGTGTGACTCTGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGT
GACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCCTGGAAAATG
TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAATGCCACACACCTGTG
GAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACAGGGAGAC
CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACATGGAACCTGCCATGAACCCAA
CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC
TCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGCACAGCCCTTCACTTAAAAAG
GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGTGAACTCCGACATCTGAAC
GTTTTAAGTTACACCAAGTTTCATAGCCTTTGTTAACCTTTTCATGTGTTGAATGTTCAAATAA
TGTTCACTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
GATATTTACTCTCTCTTTTAAAGTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCT
TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTCAGTG
TGTAAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGTGTCTGGGGCAGGGGAACAT
CAGAAAGGTTAAATTGGGCAAAATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGT
TGAAGTTACAGCATTTTCAGATTTTATTGTGAGATATTTAGATGTTTGTTACATTTTAAAAA
TTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATT
CAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTAAACAATATAATATATCTA
AACACAATGAATAGGGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATA
TATTGTAAACAAAACAGCTCTTACCTAATAAACATTTTATACTGTTTGATGTATAAAAT
AAAGGTGCTGCTTTAGTTTTTTGGAAAAA

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FIGURE 14

MARRSAFPAAALWLSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQCRNGGKIGKSKCKCSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal sequence.

amino acids 1-28

N-glycosylation sites.

amino acids 88-92, 245-249

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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FIGURE 15

AGAACCTCAGAAATGTGAGTTATTTGGGAATGGCTGTTTGTAAATGTCCTTACGTAAGCCAA
GAGGAGGTCTTGACTTGGGGTCCCAGGGGTACCGCAGATCCCAGGGACTGGAGCAGCACTAG
CAAGCTCTGGAGGATGAGCCAGGAGTCTGGAATTGAGGCTGAGCCAAAGACCCAGGGCCGT
CTCAGTCTCATAAAAGGGGATCAGGCAGGAGGAGTTTGGGAGAAACCTGAGAAGGGCCTGAT
TTGCAGCATCATGATGGGCCTCTCCTTGGCCTCTGCTGTGCTCCTGGCCTCCCTCCTGAGTC
TCCACCTTGGAAC TGCCACACGTGGGAGTGACATATCCAAGACCTGCTGCTTCCAATACAGC
CACAAGCCCCTTCCCTGGACCTGGGTGCGAAGCTATGAATTCACCAGTAACAGCTGCTCCCA
GCGGGCTGTGATATTTACTACCAAAAGAGGCAAGAAAGTCTGTACCCATCCAAGGAAAAAT
GGGTGCAAAAATACATTTCTTTACTGAAAAC TCCGAAACAATTGTGACTCAGCTGAATTTTC
ATCCGAGGACGCTTGGACCCCGCTCTTGGCTCTGCAGCCCTCTGGGGAGCCTGCGGAATCTT
TTCTGAAGGCTACATGGACCCGCTGGGGAGGAGAGGGTGTTTCTCCAGAGTTACTTTAAT
AAAGGTGTTCATAGAGT TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

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FIGURE 17

GCGAGAACCTTTGCGACGGCGACAACACTACGGGGACGATTTCTGATTGATTTTGGCGCTTTCGATCCACCCCTCC
 TCCCTTCTC**ATGGG**ACTTTGGGGACAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC
 CAGGACAGCGTCCGGGAACCGACCATGGCTCCTGGACCCCAAGATCCTTAAGTGTGTCGTCGTCGTCGCGG
 TTCTGCTGCGCGTCCGGGTGACATCTGCCACCATCCCCGGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCA
 CAGCAACAGAGGCGCAGGCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATATCTGGAGCCTT
 TAACCCGTGCA CAGAGGGTGTGGATTACACCATTGCTTCCAAACAATTTGCCTTCTTGCGTGTATGTACAGTTT
 GTAATCAGGTCAAACAATAAAAGTTTCTGTACCACGACCCAGACACCGTGTGTGTCAGTGTGAAAAAGGAAGC
 TTCCAGGATAAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTGAG
 TAATTGTACGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAAACCCAGCAG
 CGGAGGAGACAGTGACCAACATCTCGGGGATGCTTGCCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTA
 GTCATCATTTTAGCTGTGTTTGGTTTGGCTTTTCATGTGCGAAGAAATTCATTTCTTACCTCAAAGGCATCTG
 CTCAGTGTGTGGAGGAGTCCCGAACGTGTGCACAGAGTCCTTTCCGGCGCGCTTCATGTCTCTCACGAGTTT
 CTGGGGCGAGGACAATGCCCGAACGAGACCTGAGTAACAGATACTTGCGAGCCACCCAGGTCTCTGAGCAG
 GAAATCCAAGGTGAGGAGTGTGCAGAGCTTAACAGGTGTGACTGTAGAGTGGCCAGAGGAGCCACAGCGTCTGT
 GGAACAGGCAGAAAGCTGAAGGTGTGCAGGAGGAGGCTGCTGGTCCAGTGAATGACGCTGACTCCGCTGACA
 TCAGACCTTGTCTGATGCTCGGCAACACTGGAAGAAGGACATGTCAAAGGAAACAATTCAGGACCACTGGTG
 GGCTCCGAAAAGCTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCT**GTGA**AGAATCTCTTCAG
 GAAACAGAGCTTCCCTCATTTACCTTTTCTCCTACAAAGGGAAGCAGCTGGAAGAACAAGTCCAGTACTTGA
 CCCATGCCCAACAACCTACTATCCAATATGGGGCAGCTTACCAATGGTGCTAGAACCTTTGTAAACGCACTT
 GGAGTAATTTTATGAAATCTCGGTGTGATAAGCAAAACGGGAGAAATTTATATCAGATTTCTGGCTGCATAGT
 TATACGATTGTGTATTAAGGTGCTTTTAGGCCACATCGGCTGGCTCATGCGCTGAATCCAGCACTTTGATAG
 GCTGAGGCAGGTGGATTGCTTGAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAATCCATCTCAAT
 TTAAGGAAAAAAGTGGTTTTAGGATGTCTTCTTTGCACTTCTCATCATGAGACAAGTCTTTTTTCTGCG
 TTCTTATATTGCAAGCTCCATCTCTACTGGTGTGTGCAATTAATGACACTAACTACAGATGCCGCACAGCCAC
 AATGCTTTGCTTTATAGTTTTTTAACTTTAGAACGGGATTATCTTGTATTACTGATTTTTTCACTTTTCGGATA
 TTTTGGACTTAATGATGAGATTTCAAGACGTAGCCCTATGTCTAAGTCTATGAGCATATGGACTTACGAGGGTGT
 GACTTAGAGTTTGTAGCTTAAAGATAGGATTATTTGGGGCTTACCCCACTTAAATAGAGAAAACATTTATATG
 CTTACTACTGTAGGCTGTACATCTCTTTCCGATTTTGTATAATGATGAACATGGAAAAACCTTTAGGAAAT
 GCATTTATTAGGCTGTTTACATGGGTTGCCGGATACAAATCAGCAGTCAAAAATGACTAAAAATATAACTAGT
 GACGGAGGGAGAAATCCTCCCTCTGTGGGAGGCATTACTGCATTCAGTTCTCCCTCCTGCGCCCTGAGACTG
 GACCAGGGTTTGTAGGCTGGCAGCTCTCAAGGGGCAGCTTGTCTTACTTGTAAATTTAGAGGTATATAGCCA
 TATTATTATATAAATAAATATTTATTTATTTATTAAGTAGATGTTTACATATGCCAGGATTTTGTGAAGAG
 CTGGTATCTTTGGGAAGCCATGTGTCTGTTTGTGCTGCTGGGACAGTCAATGGGACTGCATCTTCGCACTTGT
 CACAGAGATGAGGACAGTGAGAATTAAATTAGATCCGAGACTGCGAAGAGCTTCTCTTCAAGCGCCATTACA
 GTTGAACGTTAGTGAATCTTGAGCTCATTTGGGCTCAGGGCAGAGCAGTGTATTATCTGCCCGGCACTCGCC
 ATGGCATCAAGAGGGAAGAGTGGACCGTGCTTGGGAATGGTGTGAATGGTGGCCGACTCAGGCATGGATGGGC
 CCCTCTCGCTTCTGGTGTCTGTGAAGTGAAGTGAAGTGGCTTGGGACAGAGATTCTTGAGCTGCGTTT
 TAGGGTACAGATTCCTGTTTGAAGGAGCTTGGCCCTCTGTAAAGCATGTGACTCATTCAGAGATATCAATTCT
 TAAACATGTGACAAACGGGATCAAAATGGCTGACACATTTGTCTTGTGACGTTCCATTTATTTTAAAA
 AACCTCAGTAATCGTTTAGTCTCTTTCCAGCAACTCTCTCCACAGTAAAGCCAGCTGGTGGTAGGATAAATTA
 CGGATATAGTCATCTCAGGGGTTTCACTCTTTTCCATCAAGGCATTGTGTGTTTTGTTCCGGGACTTGGTGT
 GCTGGGACAAAGTTAGAACTGCCTGAAGTTTCGCACATTGATGATTTGTGTGCTCATGGAGTTTAGGAGGGGAT
 GCCTTTCCGGCTCTTGCACTCTCATCTCTCCACTTCCATCTGCGCTCCACACTTGTGCTCCCTGCACTCTG
 GATGACACAGGGTGTGCTGCTCTAGTCTTGTGCTTTGCTGGGCTCTGTGTCAGGAGAGATGGTCTCAAG
 CTCAGAGAGAGCCAGTCCGCTCCAGCTCCTTTGTCCCTCTCAGAGGCCCTTCTTGAAGATGCATAGACT
 ACCAGCCTTATCAGTGTTAAGCTTATTCCTTAAACATAAGCTTCTGACACATGAATTTGTGGGGTTTTT
 GGGCTGGTTGATTTGTTTAGGTTTTGCTTTATACCCGGGCAAAATAGCACATAACACTCGGTTATATGAAA
 TACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACCTGATGCTAAGAACAACAGATATCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCTTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAATGAATGGAATTCTTAAAAA

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FIGURE 20

MRPLAGGLLKVVVFVFFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPIKERS

Important features of the protein:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

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FIGURE 21

CCGGGGAGGGGAGGGCCGTCGCCGCCCTCCCCGTCTCTCCCCGCCCTCCCCGTCCCTCCC
GCCGAAGCTCCGTCGCCGCCCGGGCCGGCTCCGCCCTCACCTCCCGGCCCGGCTGCCCTC
TGCCCGGGTTGTCCAAG**ATG**GAGGGCGCTCCACCGGGGTGCTCGCCCTCCGGCTCCTGCTG
TTCGTGGCGCTACCCGCCCTCCGGCTGGCTGACGACGGGCGCCCCGAGCCGCCCGCGCTGTC
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAACACTACACTGAAAGATGATGGGGACATAT
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAATGACTTA
CCTGTAATAGTGGTGTAACCCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAATCT
TGAAAATTTGGAGGAAAAAGAATATTTTGAATTGTCAGTGTAAGGATTTTAGTTCATGAGT
GGCCTATGACATCTGGTTCCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
GATGGAAAACAAGTTCAGCAAAAGGATGTCAGTGAAATTGATATTTTAGTTAAGAACCGGGG
AGTACTCAGACATTCAAACATATACCCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTCTC
GAGACAGTGACATTTTATTACCTTCCTAACCTCTCCAAAAAAGAAAGTGTTAGTTCAGTG
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAACCACTGTAGATGAAGATGTTTTACC
TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCGCCATCTTCATATAAGGTAATGTGTC
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTCCAGTATTC
TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT
AAAGGTGTTTTTCCAGTTTCTGAATACAAAGGAATCTTTCAGTTGGATAAAGTGGACGTCA
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA
GATAAAACATGTATT**TAA**AAGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCCTCC
AAATTTGCCACTTGAATATAATTTTCTTTAAATCGTT

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FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGSLALRLLLFVALPASGWLTTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQQKDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRDSIL
FTLPNLSKKESVSSLQTTSSQYLIRNVETTVDVLPGLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAADVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGFPEKRAENLEDKTCI
```

Important features of the protein:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

FIGURE 23

CGTCTCTGCGTTTCGCCATGCGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGG
 CCCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCGCGCCCGGTGGT
 GTTTGCTGGTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTGCAC
 CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGG
 GGAACAAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAGATTTCG
 TGCGACGGCGTGGAGTGC GGCCCGGGCAAGCGTGCCGCGTCTGGGGGGCCGCGCCGCTG
 CGAGTGC GCGCCGACTGCTCGGGGCTCCCGCGCGGCTGCAGGCTCTGCGGCTCAGACGGCG
 CCACCTACCGCGACGAGTGCAGCTGCGCGCCGCGCTGCCGCGCCACCCGACCTGAGC
 GTCATGTACCGGGGGCCGTGCCGCAAGTCTGTGAGCACGTGGTGTCGCCCGGGCCACAGTC
 GTGCGTCGTGGACCAGACGGGCGAGCGCCACTGCGTGGTGCTGTGAGCGGGCCCTGCCCTG
 TGCCCTCCAGCCCCGGCCAGGAGCTTTGCGGCAACAACAACGTCACTTACATCTCTCTGCTG
 CACATGCGCCAGGCCACCTGCTTCTTGGGCCGCTCCATCGCGCTGCGCCACGCGGGCAGCTG
 CGCAGGCACCCCTGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAACTTCGTGT
GAGCCCTGCAGGACAGGCTTGGGCTGGTGCCCGAGGCCCCCATCATCCCTGTTATTATT
 GCCACAGCAGAGTCTAAATTATATGCCACGGACACTCCTTAGAGCCCGGATTCCGACCACTT
 GGGGATCCAGAACTCCTCTGACGATATCCTTGAAGGACTGAGGAAGGGAGGCGCTGGGGGCC
 GGCTGGTGGGTGGGATAGACCTGCGTTCCGGACACTGAGCGCTGATTTAGGGCCCTTCTCT
 AGGATGCCCCAGCCCCACCTAAGACCTATTGCCGGGGAGGATCCACACTTCCGCTCCTT
 TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTGTGTGGTAATT
 CCTGAAGAGGCTAGCTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGT
 CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG
 TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGAGGATCTAG
 CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG
 GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG
 GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCCTGTGGGGA
 CCTCAGAACACTGTGACCTTAGCCACGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC
 CACCATTCCC TGCCAGCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT
 CCTGTGAAGGCCATTGAGAAATGCCAGTGTGCGCCCTGGGAAAGGGCAGCGCTGTGCTCC
 TGACACGGGCTGTGCTTTGGCCACAGAACCCAGCGTCTCCCTGCTGCTGTCCACGTCAG
 TTCATGAGGCACGTCGCTGGTCTCAGACGTGGAGCAGCCAGCGGCAGCTCAGACGAGGGC
 ACTGTGTCCGCGGAGCGCAAGTCCACTTGGGGGAGCTCTGGCGGAGCCACGAGGCCACTG
 TCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT
 CCTGGAGCCGGGTGTCCAGTGGCACCCTAGGTGCTGTGCTGCCTCCACAGTGGGGTTACA
 CCCAGGGCTCCTTTGGTCCCCCAACCTGCCCGGCCAGGCTGCAGACCCGACGCTCAGCC
 AGACCTGCCTACCCACCAATGCAGCCGGGGCTGGCGACACCGCAGGTGCTGTGCTTTGGG
 CCAGTTCTCCACGACGGCTACCCCTCCCTCCATCTGCGCTTGAAGTCCGCTACCTGAC
 TGTGCTGCGGTGAACACGACCTCAGACCAGCTATGGGGAGAGGACAACCGGAGGATAT
 CAGCTTCCC CGGTCTGGGGTGAGGAATGTGGGGAGCTTGGGCATCTCCTCCAGCCTCCTC
 CAGCCCCAGGCAGTGCCTTACCTGTGGTGCCCAAGAAAGTGCCTAGGTTGGTGGGTCTA
 CAGGAGCCTCAGCCAGGCAGCCCCACCCACCCTGGGGCCTGCCTACCAAGGAATAAAGA
 CTC AAGCCATAAAAAAA

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FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGVSSMSGGNPAPGGVCWLQQQEATCSLVLQTDVTRAEC
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPD
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCKRKSCEHVVCPRPQSCVVDQ
TGAHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEEENFV

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

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FIGURE 25

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTCTGCGGGAGCTCGTCTCCTCGTGCTGGGGT
TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT
AAAATCGCGATTATTGGAGCCGAATTGGTGGCACTTCAGCAGCCTATTACCTCGGCAGAA
ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGTTCGGGGGCCGCTTGCTA
CCATGATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCGTCAATCCATCCTTTAAATCTG
CACATGAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACT
GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA
TTAAATTAGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTG
TTAGACAAGTTCATGAGGATCTACCGCTACCACTCATGACTATGCCTTCAGTAGTGTCGA
AAAATTACTTCATGCTCTAGGAGGAGATGACTTCCTTGGAAATGCTTAATCGAACACTTCTTG
AAACCTTGCAAAAGGCCGGCTTTTCTGAGAAAGTTCCCTCAATGAAATGATTGCTCCTGTTATG
AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGCGGTGTCACTGTCCGTG
TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTCCTCAGGGCTTCTGC
AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACC
AAGTACACAGGAAATCCAACAAAGATGTATGAAGTGGTCTACCAATTTGGAAGTGTGAGACTCG
TTCAGACTTCTATGACATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTGGAATATTA
CTTTTCTCAACTTTGATCCTCCAATTGAGGAATTCATCAATATTATCAACATATAGTGACA
ACTTTAGTTAAGGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAAATTTGG
CCTTAATACAGTTTTAACCCTGATAATTTCAGATTTGTTTCATTAACAGTATTGGGATTGTGC
CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGGGAAGATC
TTTTCCCAAGAACTCTTACTAAAGCACAAATTTTAAAGCTCTTCTGTCCATGATTATGC
TGTGAAGAAGCCATGGCTTGCAATATCCTCACTATAAGCCCCGGAGAAATGCCCTCTATCA
TTCTCCATGATCGACTTTATTACCTCAATGGCATAGAGTGTGAGCAAGTGCCATGGAGATG
AGTGCCATTGCAGCCCAACCGCTGCACTCCTTGCCATCACCGCTGGAACGGGCACACAGA
CATGATTGATCAGGATGGCTTATATGAGAACTTAAACTGAACTATTGAAGTGACACACTCC
TTTTTCCCCTCTAGTTCCAATGACTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGA
TGATTTTGAACCATATTTTGCCATTATCATTGTTTAAATAAAGTAATCCCTGCTGGTCAAT
AGGAAAAAAAAAAAAA

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FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880

<subunit 1 of 1, 505 aa, 1 stop

<MW: 56640, pI: 6.10, NX(S/T): 4

MGRVVAELVSSLLGLWLLCSCGCPEGAELRAPDKIAIIGAGIGGTSAAYYLQKFGKDVK
IDLFEREVEVGRLATMMVQGGQYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLGIYNGE
TLVFEESESNWFIINVIKLVWRYGFQSLRMHMMVEDVLDKFMRIYRYQSHDYAFSSVEKLLHAL
GGDDFLGMLNRTLLETQKAGFSEKFLNEMIAFVMRVNYGQSTDINAFVGA VSLSCSDSGLW
AVEGGNKLVC SGLLQASKSNLISGSVMYIEEKT KTKYTGNPTKMYEVVYQIGTETRSDFYDI
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFLNTVLT
TDNSDLFINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKFLSYDYAVKKPWL
AYPHYKPEKCPSEILHDLRYLLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTMDIQDG
LYEKLKTEL

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

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FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQKSKKPL
MVIHHLEDCQYSQALKKVFAQNEEQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP
SLTVRADIAGRYSNRLTYEPRDLPLLIENMKKALRLIQSEL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation site.

amino acids 51-57

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FIGURE 29

TAAACAGCTACAATATTCCAGGGCCAGTCACCTTGCCATTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGACATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGA
GTGGCTGTTGGTTTCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCACTTCCAC
CAATTCCATTTCCAAGATTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9700, pI: 9.55, NX(S/T): 0

MKKVLLLTAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYFPRPLPPPIFFRFP
WERRNFPIPIPIESAPTTPLPSEK

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

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FIGURE 31

CGGACGCGTGGGCGGGCGCGCCGGGAGGGACCGCGCGCGC**ATG**GGCGGGGGCCCTGGGAT
 GCGGGCCCGTCTCGCCGCGCTGCTGCCGCTGTGTGCTGCTGCTCGGGCTGGCCCGCGGCGCCGC
 GGGAGCGCCGGGCCCCGACGGTTTAGACGCTGTGTGCCACTTGGCATGAACATGCCACATGCC
 AGCAAAGAGAAGGGAAGAAGATCTGTATTTGCAACTATGGATTTGTAGGGAACGGGAGGACT
 CAGTGTGTTGATAAAAAAGTGGCCAGTTTGGAGCCACTCTTGCTGTGGGAACACACATCT
 TTGCCACAACCCCCGGGGGCTTCTATTGCATTTGGCTGGAAGGATATCGAGCCACAACA
 ACAACAAGACATTCAATCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT
 TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG
 TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCCGACCCACCGATGCCACAT
 CATGCACAGAAATAGACTGTGGTACCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT
 TATACGTCTAGTCTGGGCAACAGGTTGCTTATGCTTGCAGAGAAGGATTCCTCAGTGTTC
 AGAAGATACAGTTTCAAGCTGCACAGGCTGGGCACATGGGAGTCCCCAAAATTACATTGGC
 AAGAGATCAACTGTGGCAACCTCCAGAAATGCGGCACGCCATCTTGGTAGGAAATCACAGC
 TCCAGGCTGGGCGGTGTGGCTCGCTATGCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA
 GATCACTTCTGTTTGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAATCATGCCAGAAA
 TTCTCAAAAGATTAATGATGTATCACTGTTTAATGATACCTGTGTGAGATGGCAATTAAC
 TCAAGAAGAATAAACCCCAAGATCTCATATGTGATATCCATAAAAGGACAACGGTTGGACCC
 TATGGAATCAGTTCTGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGACCCCAAGAGTGT
 GCCTAGCCCTGTACCCAGGCACCAACTACACCGTGAACATCTCCACAGCACTCCAGGCGC
 TCGATGCCAGCCGTATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG
 TTTCAATATTTCAATATTTAAGAACTGTTTGAATTTGAACAGCTGTGTGAGATGCCAAATGAG
 GATCAGAACACATGTACCAATTTACCCTTCTGGGTCAGAGGTGGTATCTGGCTAACTTTTCT
 CATGCAACATCGTTTAACTTTCACAAACGAGGGAACAAGTGCCCTGTAGTGTGTTGGATCTGTA
 CCTACAGCTGATTATACCGGTGAATGTGACCTGCTGAGATGCCCTAAGCGGCACATCAGTGC
 AAATAACAATAGCAACTCCCCAGCAGTAAAAAGAGCCATCAGTAACATTTAGGATTTAAT
 GAAACCTGTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGATTATTATCCA
 CATTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCAGGAAATGACCTTTAATATCAGTA
 GCAGAGCCGAGATCCCCAGGTTGTGCTTGGACCTACGCTCCGGGTACCAACTACAATGTCAGT
 CTCGGGGCTCTGCTCTCGGAATTTCTGTGGTCACTCCCTGACAAACAGATAGTACGAGCC
 TCCCTTCCCGGAAGTAGAATTTTACGGTGCACAGAGGACCTTACCAAGCCCTCAGACTGA
 GGAAAGCCAAGGAGAAAATTGGACCAATCAGTTCATATCAGTGTTTAGTGCTTCCCTGGCC
 CTCCAAAGCAATTTTCTTGTGATTCTGAAGGCGCTTCTCCTCTCTTTAGCAACGCCCTCTGA
 TGCTGATGGATACGTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA
 TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATAATGACCCCTTGAAAGAGGGAGT
 GATTACTGCATTATATTACGAATCACAAGTGAATGGAATAAGGTGAGAAGACACTCTGCTGC
 AGTTTGGGCTCAGGTGAAAGATTCTGCTACTCATGCTGCTGCAGATGGCGGTGTTGGCTGG
 GTTCCCTGGCTGTGATGATATTCTCACATTCCCTCTCCTCAGCGGTG**TCG**ATGGCAGATG
 GACACTGAGTGGGAGGATGCACTGCTGCTGGGCAAGTGTCTGGCAGCTTCTCAGGTGCC
 GCACAGAGGCTCCGTGTGACTTCCGTCCAGGAGCATGTGGGCTGCAACTTTCTCCATTCC
 CAGCTGGGCCCATTTCTGGATTTAAGATGGTGGCTATCCCTGAGGAGTACCATAAGGAGA
 AAATCAGGAATTCGAGTCTTCCCTGCTACAGGACCACTTCTGTGCAATGAACCTTGAGACT
 CCTGATGCTACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAACTTGGCTGGGAC
 TTTCTCTGAGTGTGATGCTAGGGCTCAGCTCCTCTAGACATTGACTGCAAGAGAATCTCTGCA
 ACCTCCTATATAAAAGCATTCTGTTAATTCATTAGAATCCATTCTTCAATATGCAAGT
 AGATGGGCTTAAGTTTGGGCTAGAGTTTGACTTTATGAAGGAGGTCATTGAAAAAGAGAACA
 GTGACGTAGGCAAAATGTTTCAAGCACTTAGAAACAGTACTTTTCCATATAATAGTTGATAT
 ACTAATGAGAAAATTAAGTACGCTGGCCATGCCAATAAGTTTCTGCTGTGCTCTGTAGGCA
 GCATTGCTTTGATGCAATTTCTATTGTCTATATATTCAAAAGTAATGTCTACATTCCAGTA
 AAAATATCCCGTAATTAATAA

amino acids 389-422

FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGTCTTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCCGGGCCACGCCGTCTGGAAACTCAAACGCTGAGCGTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCATTTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTG
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCTAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCGTACAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
 GGTCCCCGGGATCTGATGTCAC'TCTCCTCGTGAAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGCAGCATCAGAAATAGAAACAACAAC'TTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTACAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTG
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGACGAGTGGGCAAAACAAC'TT
 CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCT
 CTTCCCTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACG**TGAGT**GCAGGTGAAAATGGAGGTTTCTCCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAAC'TCCACGCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTCCAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAGGTTCCCATG
 AAGGGCAGCATGTCCAGCCCTTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTCACTGTTCACAGAGGTGTCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTTCAGTAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
 TTAATAATTCAC'TCAGTGTGGCCCAAAAAA

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FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722
><subunit 1 of 1, 482 aa, 1 stop
><MW: 49060, pI: 4.74, NX(S/T): 4
MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
SAETSSRASTPAGPIPEAEETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAASGS
PEGAGMTTVQITIGSDPEEAI FDTLCTDDSS EAKLTMDILT LAHTSTEAKGLSSESS
ASSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDV
TLLAEALVTVTNI EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPD
STEAKPHITEVTASAETL STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL
SGALVTVSRNPLEETSALS VETPSYVKVSGAAPVSIEAGSAVGKTTSFAGSSASSY
SPSEAALKNFPTSETPTMDIATKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKIT
TSAKTTMKPQQPRPLPGRGRPQT
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

N-myristoylation sites.amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
314-320, 349-355, 386-392, 397-403, 449-455**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

FIGURE 35

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCGGTCTGACAGCCACTCCAGAG
GCC**ATG**CCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCTGTTAATTCTGGCTTTGGGCCA
GGCAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC
CCCAGAAGTTCCAACTGTGCCTTATATCTTGAAGAAAATTTCCAGGATCGCGAGGCAGCA
GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGAATGT
ACTTCGCTTCTCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
TTGGCCCAAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA
ACTGGCTCTGTTCTCGGTCAGTGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA
AAATGTTTGTGTTGCGGTCACTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT
GTAGCTAAGGATTGGAATGACAACCCCGGAAAAATTTCTGGGTATTCTCTGGAGATACTGGT
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT
GCTCCCTTCATGCTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCCTTCTCGG
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTGAAGAACCTCTGCCACCGTCACCA
GCTATTCAATTAACCTCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTTCA
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT
TATGCTTTTCATGCAAGCCCTGATGCATGCCGTGACCCAGAGATCCCCCAGGCTGTGTGTAT
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGG**TAG**GATGTCAAGAAATGGGAAT
AGAAGGAGTGTTCTTAGGGTAAATCTTTTAATAAACTACCTATCTGGTTTATGACCCTTA
GATCGAAATGTC

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FIGURE 36

MLRFLPDLAFAFSLLILALGQAVQFQEQYVFLQFLGLDKAPSPQKFQPVPIYLKKIFQDREAAA
TTGVSRLCYVKELGVRGNVLRFLPDQGGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL
AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTFPKPGKMFVLRVWPWPQGAVHFNLLDV
AKDWNNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRK
RRAAIPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECFFSLTISLNSSNY
AFMQALMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

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FIGURE 37

CACTTCTCCCTCTCTTCTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
 CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACTTGGGTGCTCGTA
 CCGCCCCCACCCTCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTCCCTGCTCTGTT
 TCCTTACCCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
 TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGCGGGACGGAGGGCCCGCAGGAAGATGGGC
 TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCTTGCCTTTGGCTCTGGCTGGT
 CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
 CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCAGTCAG
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC
 GGGCACC GCGGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCCGCGGAG
 ATCGAGGCTCCAGGGGAATATGGCAAACAGGCTCAGCAGGGCCAGGGGCCACACTGGA
 CCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGAGCGGTGCAAGAGCCACTACGCCGC
 CTTTTCGGTGGGCGCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
 ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCCGGCAAGTTCTACTGCTAC
 GTGCCCGGCTCTACTTCTTACGCCCTCAACGTGCACACCTGGAACCAAGAAGGAGACCTACCT
 GCACATCAAGAGACAGGAGGAGGTGGTGATCTTGTCGCGAGGTGGGCGACCCGACGA
 TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGTACGCCTC
 TACAAGGGCGAACGCTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCACTTCCAG
 TGGCTACCTTGGTCAAGCAGCCACCCAGAGCCCTAGCTGGCCGGCCACCTCCCTCTGCTC
 ACCTTCCACCCCTCGCGCTGTGCTGACCCCAACGCCCTCTTCCCGCATCCCTGGACTCCGACTC
 CCTGGCTTTGGCAATTAGTGAGAGCCCTGCACACACAGAAAGCAAAGCGATCGGTGCTCC
 CAGATCCCGCAGCCTCTGACGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
 GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCAGGGC
 GAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGCGGCACCCGCGGCTCCAGTCTTGGAATA
 ATTAGGCAAAATCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGAGGACAAAGAAAGGG
 TTGTTATTTTGTCTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGCCCTTTTCGTTGAG
 ACTCTGCTTAAAGAGAAGTCCAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCGGGGGCAGG
 AAACACTACCTCTGGCTTAATTTCTTAAAGCCAGCTAGGAACCTTTCTTGAGGGATAGGTGGACC
 CTGACATCCCTGTGGCTTGTGCCAAGGGCTCTGCTGGTCTTCTAGTACACAGTGCAGGT
 GATGGGGCTGGGGCCCCAGGCTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
 TCCAGGTGTGTTAGACAGCCGAAGGGCTCCTCAGAGTGGCCAGGACCTTGGCTCCCCA
 GGCCTGCAGATGTTTTATGAGGGGCGAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
 ACCCTGTGCCACCCACAGAGCCTTGGGGGGTGGTCTCCATGCCTGCCACCTTGGCATCGGT
 TTCTGTGCGCCTCCACACAAATCAGCCCCAGAAGGCCGCGGCTTGGCTCTGTTTTT
 TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATACCCGCTT
 CCACGTGTGTGTGTTGTTGGTCAGCAAGGCTGATCCAGAGCCCTTCTGCCCCACTGCCCT
 CATCAGGCCCTTGACCATGAGCTGAGAGGGGCTTTTCTAGGCTTCAGAGCGGGGAGAG
 CTGGAAGGGGCTAGAAAGTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTTG
 AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTCTCAGGATCACTCTCAGGAGC
 TGGGTGGCAGGAGAGCAATAGCCCTCTGTGGCAATTGCAAGGACCAGCTGGAGCAGGGTTGCG
 GTGTCTCCACGGTGCTCTGCCTTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC
 ATAGCCCCCTCCACCTACCCCCATGTGATGCCCAGGGTCACTCTTGTACCCGCTGGGCG
 CCCAAACCCCGCTGCCCTCTTCTTCTCCCCCATCCCCCACTGGTTTTGACTAATCCTGT
 TCTCCCTCTCTGGCCTGGCTGCGGGATCTGGGTCCCTAAGTCCCTCTTTTAAAGAACTG
 CTGCGGGTCAGACTCTGAAGCCGAGTGTGTGTGGCGTGCCCGGAAGCAGAGCGCCACACTC
 GCTGCTTAAGCTCCCCAGCTCTTTCAGAAACATTAACCTCAGAAATTGTTGTTTCAA

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FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDGRGLQGKYGKTGSAGARGH
TGPKGQKGSMPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDERSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 39

GAATTCGGCACGAGGGAAGAAGAGAAAATACTCCGGGGCTGCTGGGAGCATATAAAGAA
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGACATGGCTG
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCCGTCCTGT
GACACTCAAGAGCTACGATGTCTGTGATTTCAGGAACACTCTGAATTCATTCCCTCTCAAAC
CATTAATAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG
TCCCAAAAAATGGGAGTATGATTTGTTTGGATCCTGATGTCCATGGGTGAAGGCTACTGTT
GGCCCAATTACTAACAGGTTCCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT
GAAGCTTCTGTATAGTGTGAGCATGAAAAGCCTCTATATCTTTTCATTTGGGAGACCTGAGA
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC
AACAGTGATAGGAATTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCCTTA
AAAGCCACTCATGAGGCAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTGGCGTTCTCA
TTCTTATACTCTATTCCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT
TATTATAAATGTTTTATTATTACTTAACCTCCTAGTGAATGTTACAGGTGACTGCTCCCCAT
CCCCATTTCTTGATATTACATATAATGGCATCATATACCCCTTTATTGACTGACAACTACT
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG
TGCATCTCGGTGTAGAGCAAGGCTCCTTGCTTCAGTGCCCCAGGGTGAATACTTCTTTGA
AAAATTTTCATTTCATCAGAAAATCTGAAATAAAAAATATGTCTTAATTGAG

FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSEFIPLKLIKIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

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FIGURE 41

CAGAC**ATG**GCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC
AGGACCCAAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT
TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGGCTGCTCCATCCCAG
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG
CTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAAGGCTGCA
AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCAT**TAG**CCCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCACCAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG
CTCAGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC
CACCCCATCTGCATTCCCAGCTCTACCTGCGCTGAGCTGCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGAGGAGAGTCTCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCTT
TGAAGGAGAATCATCAGGACCTGGACCTGATACGGCTCCCCAGTACACCCACCTCTTCCT
TGTAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCCNCCCA

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FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLLILVLAFGIPRTQGSDDGAQDCCLKYSQRKIPAKVVRSYRKQEPSLGCSIPAI
LFLPRKRSQAELCADPKELWVQQLMQHLDKTPSPQKPAQGCCKDRGASKTGKKGKSGKCKR
TERSQTPKGP**Important features of the protein:****Signal peptide:**

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTC AAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAGGCCCTTGAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

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FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST
LETIQIIKPLDVCCVTKNLLAFYVDRVFKDHPNPILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 45

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
 CTAAGCGAGGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGGCTGGGA
 CAAGAAGCCGCGCTGCTGCCCGGGCCGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
 GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG
 CCGCCGCGCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACCTCACAGCCCGCAGCGCATCCCGGTGCGCGCCAGCTCCCGCACCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGTCCACGTATGG
 ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTGCGCTTCTCGGACGCGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
 ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGTGGACTGCGCGCGGGGC
 CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
 CGTGACACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
 TCCGAGAAGCACC GGCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCCATGCTGCCATGGTCCCAGAGGAGCCTG
 AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCTGAGACCGCAGCATG
 GACCCATTTGGGCTTGTACCCGGACTGGAGGCGGTGAGGAGTCCCAGCTTTGAGAAGTTAACT
 GAGACCATGCCGGGCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGATACATATTAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGCTCTGAT
 CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCTGGGCCCCCATTTCTGCTCCCTCGA
 GGTGTGCTGGACAAGCTGCTGCACGTGCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
 TCACTTCCTTTGGAAAAATTCCTATGTCAAGCTGAAATTCCTAATTTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTCAAGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCACTTCCAGGG
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAAGTGAAGTGGAGCAGGCATGGCCACCAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC
 CTGAGGCCAGTTCTGTGTCATGGATGCTGTCTGAGAAATAACTTGCTGTCCCGGTGTCACCTGC
 TTCCATCTCCAGCCACAGCCCTCTGCCCCACTCACATGCTCCCCATGGATTGGGGCCT
 CCCAGGCCCCCACTTATGTCAACCTGCACCTCTTGTTCAAAAATCAGGAAAAGAAAGAT
 TTGAAGACCCCAAGTCTTGTCATAAAGTGTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
 CCTTTCCCGCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATATTTTATGCCCCCAATTATATTTATGTATGTAAGTGAGGTTG
 TTTTGTATATTAAGTGGAGTTTGTGTTG

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FIGURE 46

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLEIKAVALRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSAQKQQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 47

GTCTGTTCCAGGAGTCCCTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATATGGTCTCTGAGGAAGCGGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTGACCACCATGGGAACCGGG
CAGTGCTGACATGCTCAGAAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTTTCCTATGTCCT
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCCGTGCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTATCGTGGCAGCCGTCTTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTCTGGTGTGAGGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCTTACT
CAGGTGCTACCGGACTCTGCCCCCTGATGTCTGTAGTTTACAGGATGCCATTATTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTACAGTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCACCTGCTGAGTGGCCTGGAACTGTTTTAAA
GTGTTTTATTCCCCATTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACCTCACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTCCCTTGTTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGGTCTCTCCATCTCTGGGGCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTGAAGCCAAAAG
GATTTAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCAGAGGCTGAGGCAGCGGATCACCTGAGGTGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAATACAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAA

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FIGURE 48

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTTRLVCYNNKITASYEDRVTFLEPTGITFKSVTREDTGTYTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNIPISSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPTSNAVRMEAVERNVGVIVA AVLTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 49

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCGCCGCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAAACCTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCCGGGCGTCGCATCTCCGCCACGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACAGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCAACCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTGGGCCGCCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGGAAGCATCCGAGCCCCAGCTGGGAAGGGGAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGCCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTGTTGTTTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCACGACCCAGGCGCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTCCTGCG

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FIGURE 50

MGAARLLPNLTLCLQLLLIICCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTEIVLENNYTAFQNAHREGWFMAFTRQGRPRQASRSRQNRQEAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 51

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAAAACCAGACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCTCAGGTGCATATT
GACAACCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCCTGGATCCTCGCGTGGTCCCTTCTGAGCAACACCCAAACGAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATGTAGAGATTTC
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTACCCGTGAACATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGAATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACGAACCAATCAGATATATACAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGAGATATTTAGGTACAATGGAGTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGAGACCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACCTTGGTAGACTGTGCCACCACGGCGTGTGTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

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FIGURE 52

MKTIQPKMHNSISWAIFTGLAALCLFQGVFVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNIRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVRVKVTVNYPPYISEAKGTGVPVGQKGTQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCAASNKLGHNTASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

Signal peptide:

amino acids 1-28

[illegible]

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FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALCLGSGEAGPLOSGETGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDEVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAIPWQGGNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGGSGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSS
GSSSTGSSSGNHGSGSGGNGHKGPCCEKPGNEARGSGESGIQGFQGVVSSNMREISKEGNRLL
GGSGDNYRGQGSWSGGGDAVGGVNTVNSSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

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FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCAGCTCAGCA**AATG**GCAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGGGCTGCACAACTGAC
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCTGGCCCTGCTCTCCAGTCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAATGATGTTAAAGTAAGAATTGCAAAA

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FIGURE 56

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop,
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFVVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

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FIGURE 57

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG
 GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGGTGA
 GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCCTTGCCCGCCAACCGGTTGCAG
 GCGGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACAGGGGAGGTGTCTTC
 ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCCTCAAACAGAAAAGGAGGATC
 AAGTGTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
 ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTTA
 CAGTGTCTCCGTGAATGTGCAAGACAAACAAGGCAAAATCAGGGGCCACAGCATCAAAACCT
 TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
 GTGGGGGCAAAAGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGTGTCCAATACCA
 GTGGGATCGGCAGCTTCCATCCTTCCAGACTTCTTTGCACCAGCAATAGATGTTCATCCGTG
 GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
 AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGTGC
 AGTGGTTGCTGGAGCTGTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
 TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
 ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
 TTCTCTGTCACTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGAT
 TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAGACTGCCACGACAGAT
 GGGGCCACCTCAACCAATATCCCCATCCCCGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
 CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC
 CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC
 AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
 TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
 AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
 CTGAAATTAGCTACTCACCAAGAGTGAGGGGAGAGACTTCCAGTCACTAGTCTCCAGGC
 CCCCTTGATCTGTACCCCAACCCATATCTAACACCACCCCTTGCTCCCACTCCAGCTCCCTGT
 ATTGATATAACCTGTCAGGCTGGCTTGGTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
 TTATTAAACTAACATGAAATATGTGTGTTTTCATTGCAAAATTAAATAAAGATACATAA
 TGTTTGTATGAAAAA

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FIGURE 58

MISLPGLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVFPVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPPWPKSSDTISKNGTL
SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

FIGURE 59

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCGAT
 CATTTTGATTTTGGCTGTTTATTTTTTTTTTCTTTTTCTTTTTCCACCACATTGTATTTTAT
 TTCCGTACTTCAGAAATGGGCTTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTCTCT
 GAAGTCTTTGGCTTATCATTTCCCTGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
 CTAGTGTGTGCCGTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACCAAAATTAATAATGC
 TGGATTTCTCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTTCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAAC
 AATATTCAGACCATTTTACGCGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
 TCAAATTTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCAATATCCGACATGGCCTTCCAGAA
 TCTCAGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAGGGTATCGCGG
 AGGGCACCTTCAGGCATCTCACCAAGCTCAAGGAATTTTCAATTACGTAATTGCTGTCC
 CACCTCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTCAGGACAAACAGAT
 AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTTCCAACTTGAAGCAGCTC
 ACTGCTCGGAATAACCCCTTGGTTTTGTGACTGCAGTATTAATAGGCTCAGAGAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGTCTTGAACAGCTCGGG
 GGATGGCCGTGAGGAATTAATATGAATCTTTTGTCTGTGCCACACGACCCCGGGCTG
 CCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCTCTCTAT
 TCCAAACCTTAGCAGAAGCTACACGCTTCAAACCTCTACCACATCGAAACTTCCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCATTCAAGTCAGCTGGCTCTCTCTTACCCTGATGGCATA
 CAAACTCACATGGGTGAAAATGGGCCACAGTTTGTAGTGGGGGCATCGTTAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTAGTGCCACTCGGCTGCTTTAACTACCGCGCGTAGAAGACACCATTTGTTTCAGAGGC
 CACCAACCATGCTCCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCATGAGCAGAGCA
 CGTCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGCTTGATCGGGGGCGCGGTGATATT
 GTGCTGGTGGTCTTGTCTCAGCGTCTTTTGTCTGGCATATGCACAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAAAAACAACCGGGGCGGGCGGAAGATGATTATTGCGAGGCAGGCACCAAGA
 AGGACAACCTCCATCTGGAGATGACAGAAACAGTTTTTCAGTACGTCTCCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTCAGACTGCAGCCATTTACACCCCAATGGGGGCATTAATTA
 CACAGACTGCCATATCCCAACAACATGCGATGCTCAACAGCAGCGTGCCAGACTGGAGC
 ACTGCCATACGTGACAGCCAGAGGCCCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACCGGTGACTATATAATGGGATTAAAAAAGTG
 CTATCTTTTCTATTTCAGTTAATTACAAACAGTTTTGTAACCTTTTGTCTTTTAAATCTT

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FIGURE 60

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFMNLPKNVRLHLQENNIQTI
 SRAALAQLLKLEELHLDNDSISTVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDLQELR
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPD
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
 PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMVRELNMNLLSCPTTTPGLPLFTP
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLFTIPDWDGRERVTPPISERIQLSIHFVND
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
 LSVFCWHMHKKGRYTSQKWYKYNRGRKKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
 DFRLQPIYTPNGGNYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 61

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGCAACTGTTATTTACTGTCGCGTTT
 TAGTTGGGGAATTCCTCTCCTATGGCCCTTGTCCTGGAGCAACAGAAAACCTCTCAAAACAAGA
 AAGTCAAGCAGCCAGTGCAGTCTCATTGGAGTGAAGCGTGGCTGGGTGGAAACCAATTT
 TTTGTACCAGAGGAAATGAATACGACTAGTCAATCAGTATCGGCCAGCTAAGATCTGATTTAGA
 CAATGGAAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAAGTACTTTTATCA
 TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCCATCCCTC
 TACATCTTAAGAGCCCAAGTAATAGACATCGCTACTGGAAGGGCTGTGGACCTGAGTCTGA
 GTTTGTCATCAAAGTTTCCGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
 AGGCCATTGTACCAGAGATGTCCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
 GCTGACGATCCCTCAAGTGGTAATAATGTCGTCCTCTACAGCTTACTTCAAGGCCAGCC
 ATATTTTCTGTTGAACCAACAACAGGAGTCAATAAGAATATCTTCTAAAATGGATAGAGAAC
 TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
 TCTGGAACAACAAGTGTATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAA
 AGAAAGTTTATACCCTTGACTGTCCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
 TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTTGAAGAGCA
 GATTCGCAAAACATTGACATTATTAATACTAATGAACTCAAGAAGAAATAGTTATATTTAA
 AAAGAAAGTGGATTTTGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAAACCATC
 ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAAGATCCAG
 GTGGAAAGATGTTGATGAGCCCTCCTCTTTTCTCTCCATTAATGATTATTTGAAGTTTGTGA
 AGAAACCCCCACAGGGATCATTTTGAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
 CTCTATCAGGTATTTCTATTACTAGGAGCAAAAGTGTTCATATCAGATGATAATGTTACAATC
 ACTACAAGTAACCTACTGGATCGTGAAATCAGTGCCTTGGTACAACCTTAAGTATTACAGCCAC
 AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAAACATCA
 ATGATCATGTCTCCTGAGTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
 GGTCAAGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAAGAGCACCATTT
 TTACTTTAATCTATCTGTAGAAGACACTAACAAATTCAGTTTACAAATCATAGATAATCAAG
 ATAACACAGCTGTCAATTTGACTAATAGAAGTGGTTTAACTTTCAGAAGAAGCTGTCTTC
 TACATCTCCATCTTAATTCGCCGACAATGGAATCCCGTCACTTACAAGTACAACACCCCTTAC
 CATCCATGCTGTGACTGTGGTGACAGTGGGAGCACACAGACTGCCAGTACACAGGAGCTTG
 TGCTTTCCATGGGATTCAGAGCAGAAGTTATCATTTGCTATTCTCATTTGCAATATGATCATATA
 TTTGGGTTTATTTTGTGACTTTGGGTTTAAACAACGGAGAAAACAGATTCATTTCTCTGA
 GAAAAGTGAAGATTTTCAGAGAGAATATATTCCAATATGATGATGAAGGGGTGGAGAAGAG
 ATACAGAGGGCCTTGTATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
 CGGAAAACCAACGAGCTGAGATCAGGAGCCTATACAGGCATGCTTTGCAAGTTGGCCCGCA
 CAGTGCCATATTTCAGGAATTCATTCTGGAAGAGCTCGAAGAGCTAATACCTGATCCGCTGTG
 CCGTCCCTTTTGATTCCTCCACACCTACGCTTTTGAGGGAACAGGGCTATTAGCTGGATCC
 CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
 GGGACCTCGCTTTAAAGATTTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAAATTAATAG
 GCTTTTACCATCAAAATTTTAAAGTGCTAATGTGATTTCGAACCCAATGGTAGTCTTAA
 AGAGTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTCTGATTCC
 CTGGAGTAAATACCTCATGGTTATTTAAGCTACCTACATGCTGTCATTGAACAGAGATGTG
 GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAAGTTTGAAGTAAAAATAG
 TAGGAAGATATTAAGAGTAGATGAGAGGACACAGATGTAGTCGATCCTTATGCGATTATAT
 CATTATTTACTTAGGAAGAGTAAAAATACCAACAGAAAATTTAAAGGAGCAAAAATTTG
 CAACTCAAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
 ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCTTTAT
 TTAATA

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FIGURE 62

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLRLRMLGIPLLWPCLGATENSQTKVKQPVRSHLRVKRGVWVNQFFVPEEMNTTSHH
IGQLRSDLNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAI VPMSPEGTLVIQVTASDADD PSSGNNARL
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVD FEHQNHYIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVD EPPFLFL
PYVVFVEFETPQGSFVGVSATDPDNRKSP IRYSTRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDH APEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHFYNLSVEDTNSSFTIIDNQDNTAVIL TNRTGFNLQEEP VFYISILIADNGIP
SLTSTNTLTIHVCD CGDSGSTQTCQYQELVLSMGFKTEV IIAILICIMII FGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDS AIFRKFILEKLEANTDPCAPPFDSLQTYAFEGT GSLAGSLSSLES AVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN
```

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCA**AATGGC**
CGCCCTGCAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGAC
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACCTTCACCTTGAGAAGTGCTGTTTC
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCTTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTG
GATTTGCTGTTTATGCTCTCTGAGAAATGCCTGCATT**TGACC**GAGCAAAGCTGAAAAATGAA
TAACTAACCCCTTTCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC
CAAAAGGAAGATGGGAAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTCTTAAGCA
TAGATATTTATTGATAACATTTTCATTGTAACCTGGTGTCTATACACAGAAAACAATTTATTT
TTTAAATAATTGCTTTTTTCCATAAAAAAGATTACTTCCATTCCCTTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATATTATTA
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTATTATATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

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FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185
><subunit 1 of 1, 179 aa, 1 stop
><MW: 20011, pI: 8.10, NX(S/T): 3
MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI
```

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

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FIGURE 65

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGA
 CGCGCGCCCTGCGTCGGGGCGAAGAAAAGAAGCAAACTTTGTCGGGAGGGTTTCGTCATCAAC
 CTCCTTCCCAGCAAACTTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAGTTCTCTGCA
 GAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGCGCTGGCTGTGGAATTAGATCTGT
 TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCAACCGTCCGCGGGCACC GG GTTGG
 CGCTGCCCGAGTGGAAACCGACAGTTTGCAGGCTCGGTGCAAGTGGCCCTCTCTCCCGCG
 GTTGTGTGTTCACTGTCGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAGAGAGAGCTCAGAGG
 TCCGAAGAGCGCTGCGCTCTTACTGCGGTTGCTTCTTCTCTCTCGGTTCCCTACTGTGA
 AATCGCAGCGACATTTACAAAGGCTCCGGGTCCTACCGAGACCGATCCGCGAGCGTTTGCC
 CGGTCTGTCCTATTTGCATCGGGAGCCCCGAGCACCGGCGAAATGCGCAGGTTCCCGAAGGC
 CGACCTGGCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTCACGGACCAAGTTTCAGTTTCG
 CCGATGGGAACCCGGAGACCAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCT
 CACACAGAGGAGGAGGTGGAAGTTGATTACACACGCGTACAGCCACAGGTGGAAGAAAGAACTT
 GGACTTTCTCAAGGCGGTAGACACGAAACCGAGCAAGCGTCGGGCAAGACTCTCTGAGCCCA
 GAAGCTTTCACAGACTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT
 ACAGACCACAATTACTATCTCGAATATATGGTCCATCTGATTCTGCGCAGCGGGGATTT
 ATGGGTGAACATAGACCAATGGAAGAAAGATAAAGTGAAGATTTCATGGAATATTGTCCAATA
 CTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGCCACTTCTTA
 CGTGAAATCACTGTGGCAACCCGGGGTTTCATATACACTGGAGAAAGTCGTACATCGAATGCT
 AACAGCCACACAGTACATAGCACCTTTAATGGCAAAATTCGATCCAGTGTATCCAGAAAT
 CAACTGTAGATATTTTGATAATGGCACAGCACTTGTGGTCAGTGGGACATGATACATCTC
 CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCTGCTCATGGATGGACGAAT
 CATCTTTGGATACAAGAAATTCCTGCTTGGTCACACAGATAAGTTCAACCAATTCACAG
 TGAAGTCGGACTGTCCGATGCATTTGTGCTTGTCCACAGGATCCAAACAAATTCCAATGTT
 CGAAGAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTTACCAACAT
 TTCCGCTGTGGAGATGACCCCAATTACCCACATGCCTCCAGTTTAAACAGATGTGGCCCTGTG
 TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAAACTTCAAAGATGTTCCAGTGGA
 TTTGATCGTCATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGAT
 GTGTGAGAAATACAGAACCATGTGGAAACTTCTTCTCGAACCCACCAACCGTAGGAGCGACAA
 CCACCCAGTTAGGGTCTCTAACTACCACCAGAAGAGCAGTGACTTCTCAGTTTCCACACGC
 TCTCCTACAGAAATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGA
 TGACAGTGCAGCTGAGAAGAAAGGGGAACCTCCACGCTGGCCTCATCATTGGAATCCTCA
 TCCTGGTCTCTATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCAACA
 TCAGCAGCCAGCATCTTCTTTATTGAGAGAGCCCAAGCAGATGGCCTGCGATGAAGTTAG
 AAGAGGCTCTGGACATCTCTCCCTATGCTGAAGTTGAACCAAGTTGGAGAGAAGAAGGCTTTA
 TTGTATCAGAGCAGTGTCTAAATTTCTAGGACAGAACAACACCACTGCTGGTTTACAGGTGT
 TAAGACTAAAATTTTGCTTATACCTTTAAGACAAACAACAACACACACAACAACAGCTC
 TAAGCTGCTGTAGCCTGAAGAGACAAGATTTCTGGACAAGCTCAGCCACAGGAAACAAGGG
 TAAACAAAAAATAAACTTATAAAGATACCATTTACACTGAACATAGAATTCCCTAGTG
 AATGTCATCTATAGTCACTCGGAACATCTCCGCTGGACTTATCTGAAGTATGACAAAGATTA
 TAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAGGGATCAGAAAAAAATCATATAAAGC
 TTAGTTTCATGAGG

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FIGURE 66

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVQTQAFPHTEEVEVD SHAYS
HRWKRNLDFLKAVDTNRSVVGQDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYYSIRIYGPS
DSASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNSFDFPFYGHFLREITVATGGFIYTG
EVVHRMLTATQYIAPLMANFDPVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQAT
LLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEHVRELQ
MSKITNISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSSWCSKLQRCSSGFDHRHQDWVDSGCP
EESKEKMCENTEPVETSSRTTTTVGATTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLK
DNGASTDDSAAEKKGGLHAGLIIGILILVLI VATAILVTVYMYHHPTS AASIFFIERRPSR
WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQ

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

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FIGURE 67A

GCAGCCCTAGCAGGGATGACATGATGCTGTTGGTGCAGGGTGCTTGTGTGCTCGAACCAGTG
 GCTGGCGGGCGGTGCTCCTCAGCCTGTGCTGCTGCTACCCCTGCTGCTCCGGGTGGACAGA
 GTGTGGACTTCCCCCTGGCGGCCGTGGACAACATGATGGTCAGAAAGCCGGACAGCGCGGT
 CTTAGTGTTATTATTGGAAGATGGAGCTTCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTAT
 TTTTGGCGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
 GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACAGCGTGTCT
 GTTCAGACTCAACATACACCCAGAACATGCAGGTGCATCTAACTGTGCAAGTTCTCTCTAA
 GATATATGACATCTCAATATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGT
 TGGCCACTGGGAAACCAGAGCCTTCCATTCTTGGCGACACATCTCCCCATCAGCAAAACCA
 TTTGAAATGGACAATATTTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAAATATGA
 ATGCAGTGCAGAAAATGATGTCTATTTCCAGATGTGAGGAAAGTAAAGTTGTTGTCAACT
 TTGCTCCTACTATTAGGAAATTAATCTGGCACCGTGACCCCGGACGCGAGTGGCTGATA
 AGATGTGAAGGTCAGGTGCGCGCTCCAGCCTTTGAATGGTACAAGAGGACAGAAGACT
 CTTCAATGGCCAAACAGGAATTATTATTCAAATTTTAGCACAAGATCCATTCTCACTGTTA
 CCAACGTGACACGAGGACACTTCGGCAATTATCTTGTGTGGCTGCCAACAGCTAAGGCACA
 ACCAATTGCGAGCGCTGCTCTTAACCCCTCAAAGTACAGCCAGTATGGAATTACCGGGAGCGC
 TGATGTCTTTTCTCTGCTGGTACCTTGTGTTGACACTGTCCTCTTACCAGCATATCTCT
 ACCTGAAGAATGCCATTCTACAATAAATTCAAAGCCCATAAAGGCTTTTAAGGATTCTCT
 GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAGCAGCGTGGGATATACT
 AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATATTGTAATACTTTTAA
 GTTCTTTTGTATAGTACATTACCTTGTGAAGCAGTACACATTGCTCCTTTTAAAG
 ACGTGAAGCTCTGAAATTAATCTTTAGAGGATATTAATTGTGATTTCATGTTTGAATCTAC
 AACTTTTCAAAGCATTCAGTCATGGCTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAA
 TATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTCAGTTCCTGTTCAAT
 AAGAGTCAATCCACATTATCAAAAGATGCAATTTTCTTTTGTATAAAAAGCAATAATA
 TTTGCCTCAGATTATTTCTCAAATAATAACACATATCTAGATTTTTCAGTCGATGATAT
 TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTCTCTCTCTGT
 AAGTTTCAGCATGGGTGCTCCTTATACAAATAATATTTTCTCTTGTCTCCAACATATAAA
 AATGTTTTGCTAAATCTCAAAATTTGAAAGTAAAAATAAACAGAGTGATCAAGTTAAACCA
 TACACTATCTTAAGTAACGAAGGAGCTATTGGACTGTAATAATCTCTTCTGCATGACAA
 TGGGGTTTGAGAAATTTGCCCCACATACTCAGTCTTGTGATGACAGACAATTAATAAC
 AGTATAGTAAATATACCATTGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA
 AATCATCTCCCTTTAAATATGACAGCACAGTCCACTCAAAGGATTGCTAGCAATACAGCATCT
 TTTCTTTCACTAGTCCAAGCCAAAAATTTAAGATGATTTGTGCAAAAGGACACAAAGTCC
 TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTAATTTTATTTTGGGACGCTAA
 GTTAGATGACAGAGCGAGTGTCTCTGTGGACAGGAGCATTTTGCATTTTCTCATCTGAAA
 GTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACTTCCAAAATATATTA
 TAACAAACATCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTTCTCAATAA
 AATCTTTCTATATAGCCATTTCACTGCAAAACAAGTAAAAATCAAAAAGACCATCCTTTATT
 TTCTTTACATGATATATGTAAAGTGCATCAAAATAAGACAAAACACCGATGATGAGAATAT
 CTTAAGATAAGTAATATTAAGATTTTGTGAATGTTAAATTTTCTACTATAAAGAACGAA
 AACTACATTTTTGAAGGAAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGG
 TTTCACTCTTTACTAAAGAAAGGCCATCACCTTTGAAAGCCATTTTACAGGTTTGTGAAGTT
 ACCAATTTCACTAGCACTAAATTTCTACAAATAGTCCCTTTTACAAGTTGTAACACAAG
 ACCCTATAATAAAATTAGATACAAGAAATTTGCAGTGGTTATACATTTTGAGATATCTAG
 TAGTTTGCCCTAGCAGGATGGCTTAAAAACTGTGATTTTCTTCAAGTAAACTAGT
 CCCAAGTACATCAATAATCAATTTAATTAGAAAAATGAATCTTAATGAGGGACATAG
 TATACTCTTTCCACAAAATGGCAATAATAGGCATAAAGCTAGTAAATCTACTAAGTGAAT
 AAATGTATGACATTAATTTGATTTGATACATATAAAAAAGAGTTTGTGAACAAACATAGGCAT
 TAACCTTTATTATTATTGCTTTTAAAGAAATATCTTTGTGGAATTGTTGAATAAATATAA
 AATATTATTTGTATTGCAGCTTTAAAGTGGCACACTCCATAATAATCTACTACTAGAAAT

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FIGURE 67B

AGTGGTGCTACCAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
 AAGAATGCATATTATTCAGTGACCGCTTTCCTAGAGTTAAATATCCTCCTCTTTGTAAGGTT
 TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTGTCATG
 ATTCCAAATTTGTGGAGCTCGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
 CAGTAGCTATATGTATTTGCCTTTATGTTAGAAGAGACTTCTTGAGTGACATTTTAAATA
 GAGGAGGTATTCACATATGTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA
 CAGAGTGAAATCATGAGTATTTATGAGTTCATATTTGTCAAATAAGGCTACAGTATTTGCTT
 TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA
 AATGTCCTGATTACCCCATTTTATCAGTCTGACTGTACAAGATTGTTGCAATTTTCAGAATAG
 CAGTTTATAAAATTGATTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTTCAATTCAGG
 ANTATATTTTCTACAAGTCCACTTGTGGGACTCCTTTTGTGCCCCATTTTTTTTTTAAAG
 AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAAGAAAAGAAATG
 AAAAGGAAAGGCAGTAAAGAGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
 AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGGAAGGAAGAATCAGAGTATTAGG
 GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGAACATATGTTTTCAA
 TGATCGCATTTGAACATAAGTCCATTATACCATTAAAGTTCCTATTTATGCAGCAATTATAT
 AATAAAAAGTACTGCCAAGTTATAGTAAATGTGGGTGTTTTTGAGACACTAAAAGATTGAG
 AGGGAGAATTTCAACTTAAAGCCACTTTTGGGGGGTTTTATAACTTAACGAAAAATTAATG
 CTTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGGAACTGAGAAAAATTACCCAG
 GTAATTCAGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
 ACTCTGAAAACTGAATTATCAAGTCAATCATCTATAATGATCAAATTTACTGAACAAATTG
 TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
 AAAAAAATTGTTTTGAAATCCAGAAATGATTTAAAGAGAGGTACGGTTTTTACTATTTA
 TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
 GATTCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA
 CATCCATATTTATAACCTGATGTAAAAATATGTTGACTGTTTCCAATAGGTGAATATAAAC
 TCAGTTTATCAATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 68

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259

><subunit 1 of 1, 354 aa, 1 stop

><MW: 38719, pI: 6.12, NX(S/T): 6

MDMMLLVQGACCSNQWLA AVL LSLCCLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYL
EDGASKGAWLNRSSII FAGGDKWSV DPRVSI STL NKR DYS LQIQ NV DVTDDG PYTCSVQTQH
TPRTMQVHLTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQ
YLDIYGITRDQAGEYECSAENDVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGA
GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQE HFGNYTCVAANKLGTTNASL
PLNPPSTAQYGITGSADVL FSCWYLVLTLSSTSI FYLKNAILQ

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.

amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
304-310, 321-327

Myelin P0 protein.

amino acids 94-123

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FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACA
ATTTACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTG
TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAAGCTTCTCCAGAAGCA
AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT
TTAATTAAGGGTTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT
GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGAC**ATG**TATAGACACAAAAA
CAGCTGGAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAA
CATTGATTTTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA
GCCCACAAGATGCCATTGTCCCCCGGCCTCCTGTGCTGCTGCTCTCCGGGGCCACGGCCAC
CGTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGTGGTTTGAGTGGACCTCCAG
GCCAGTGCCGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC
ACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAAGTCTTCTGGAAGACCT
TCTCCTCCTGCAAA**TAG**

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FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175
><subunit 1 of 1, 155 aa, 1 stop
><MW: 17194, pI: 10.44, NX(S/T): 0
MYRHKNSWRLGLKYPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK
```

Important features of the protein:

Transmembrane domain:

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

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FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCT**ATGG**CGTGGAGCCTTGGGA
 GCTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTC
 AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG
 GAACCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTTCCAAGATAAATGCATGAATA
 CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC
 AGGGCTGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCTGTGGATGA
 CACCATTATTGGACCCCCCTGGAATGCAAGTAGAAGTACTTGTGATTCTTTACATATGCGTT
 TCTTAGCCCCCTAAAATTGAGAATGAATACGAAACTTGGACTATGAAGAATGTGTATAACTCA
 TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTTACTCCCCA
 GTATGACTTTGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTCAAGTTTCGAG
 GGTTTCTTCCTGATCGGAACAAAGCTGGGGAATGGAGTGGCCCTGTCTGTGAGCAAAACACC
 CATGACGAAACGGTCCCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGT
 CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGTCTGTGGTGGCTTTACAAGAAGACAAAGTACG
 CCTTCTCCCCTAGGAATTTCTCTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT
 AACACACTTCTGTTTTTCTCCTTTCCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAG
 GTGCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA
 CCCCCTGGGCGAGGGGCCCAAGCT**TAGG**CTCTGAGAAGGAAACACACTCGGCTGGGCACA
 GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAAACAAGGGCCAAGA
 CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT
 TTTAAAGGCTGTCTTGGCAAAAATACTCCATTTGGGAACCTCACTGCCTTATAAAGGCTTTCA
 TGATGTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTCAGCCTTTTATATCACATAAAATAA
 GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCAGGCCTGTAATACCAGCA
 CCTTAGAGGTGAGGCGAGGCGGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCATA
 TGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTAT
 AATCCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA
 GGTGTCAGTGAGCCGAGATAGCGGCACCTGCACCTCCAGCCTGGGTGACAAAGTGAGACTCCAT
 CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACCTTAAATGAGGAATAAGAAATGG
 AGATGTTACATCTGGTAGATGTAACATTCTACCAGATTATGGATGGACTGATCTGAAAATCG
 ACCTCAACTCAAGGTTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGGATTCTTTGCA
 GTACTTTGAATTTATTTTCTACCTATATATGTTTATATGCTGCTGGTGTCTCCATTAAGT
 TTTACTCTGTGTTGC

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FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSAALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFIQITPQYDFEVLRLNLEPWTT
YCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVPSSWMVAVILMASVFMVCLALLGCFSLWCV
YKTKYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESQKQNP
DSCSLGTTPPGQGPQS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

FIGURE 73

CGAGCGCCAACCCGCTAGCGCCTGAATCCGGCGTGCTGCCGCGCTCGCCGCCCGCCCATGCGCCC
 GCGCAGCCCCGCTGCTCGCCGCGCTTGACCGCGCTCCTCGCCGCGCGCCGCTGCTGGCGGAGAT
 GCCCGCGCGGCAAAATCGCGGTGTTGGGGCTGGGATTGGGGCTCTGCTGTGGCCCATTTT
 TCTCCAGCAGCACTTTGGACCTCGGGTGCAGATCGACGTGTACGAGAAGGGAACCGTGGGTG
 GCCGCTTGGCCACCATCTCAGTCAACAGCAGCACATATGAGAGCGGGGCTGCCTCCTTCCAC
 TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGCTGAGGCACCGCGCGAGGT
 GGTGGGCAGGAGGCCATCTTCGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC
 TGCTGAACCTCTTCCGCTCTGGTGGCACTATGGCATCAGCTTCCCTGAGGCTGCAGATGTGG
 GTGGAGGAGGTCTATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCCACGGCTATGCCTT
 CTCGGGTGTGGAGGAGCTGCTCTACTCACTGGGGGAGTCCACCTTTGTTAACATGACCAGC
 ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCAAGCAGCGCTTTATTGATGATGTCGTT
 TCTGCTGTCTCGCGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCTTTGCAGGAGCCAT
 GTCATGACCGGGGCCCAAGCGAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGGTGTGTT
 CCGGTTTGCTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTGACCTCTGTGACCCTG
 CACAGCACAGAGGGGAAAGCCCTGTACCAGGTGGCGGTATGAGAATGAGGTAGGCACAGCTC
 TGACTTCTATGACATCGTGGTCAATCGCCACCCCTGCACCTGGACAACAGCAGCAACT
 TAACCTTTGCAAGCTTCCACCCGCCCATTTGATGACGTGCAGGGCTCTTCCAGCCACCGCTC
 GTCTCCTTGGTCCACGGCTACCTCAACTCGTCTACTTCCGTTTCCCAAGCCCTAAGCTTT
 CCCCTTTGCCAACATCTCTTACCACAGATTTCCCCAGCTTCTTCTGCACTCTGGACAACATCT
 GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCAGCTGTTTGGCGA
 GTCAGTCCCCCAAGCCCTCTTTCCGGACCCAGCTAAAGACCTGTTCCGTTCTTATTACTC
 AGTGCAGACAGCTGAGTGGCAGGCCCATCCCCTCTATGGCTCCCGCCCCAGCTCCCCAGGT
 TTGCACTCCATGACCAGCTCTTCACTCAATGCCCTGGAGTCCGTTTCCCAAGCCCTAAGCTTT
 GTGATGGCCGTGGCTGCCAAGAAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT
 AGACAAGATTGATCAAAAAGATTTGATGCACAAGGTCAAGACTGAAGTGTGAGGGCTCTAGG
 GAGAGCCTGGGAACCTTTCATCCCCACTGAAGATGGATCATCCACAGCAGCCAGGACTGA
 ATAAGCCATGCTCGCCACCAAGGCTTCTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG
 ACCTACTGCTGCCATATTAAGGGTCCACACGCGCGCTGCTGCTTTTTTTTTTAAAGGGGAAA
 GTAAGAAAAGAGAAGGAAATCCAAGCCAGTATATTTGTTTTATTTATTTTTTTTAAAGAAGAA
 AAAAGTTTCATCTTCAAGGTGCTTCAGACTTGGTTTCTTAGCTAGAAACCAAGAGACTACG
 GGAGGGAATATAAGGCAGAGAATATGAGTCTTATTTTATTACTGTTTTTCACTACGACTATC
 CCACAATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAACCAAGATGGTTACAAA
 TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCTGGTTACTGTGAGCT
 TGATGGATTGAAGTACCTAGTTCTCAGAACTCCCTAGTCACTCTCCAAGCCCTGCAACATC
 ACTGCATATTGGAGGAGATGACTGTGGTAGGACCCAAAGGAAGAGATGTGTCCTGAATAGTC
 GTCACCATATCTCAAGCTTCTGGCAACCAAGTGGGAAAAGAAACATGCGAGGCTGAGGAA
 GAGGGAAGCTCTTCTTGGCACCTAGAGGAATTAGCCATTCTCTTCCTTATGCAAGATTGA
 GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGGTAGAGAGCAGTATATCTTACCCC
 TAGATGTTTATCCCCAGCAGAAGAAAGAAGAGGTGTTGGGGTAGGATTCTTCAGAGGTTAGC
 CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTT
 TTCTACAAACCTTAAAAATCACTTGTTTAAAAAGAAGTAAAAGCCCTTTTCATTCAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510
><subunit 1 of 1, 494 aa, 1 stop
><MW: 54646, pI: 7.27, NX(S/T): 6
MARAA PLLAALTALLAAAAAGGDAPPGKIAVVGAGIGGSAVAHFLQQHFGPRVQIDVYEKGT
VGRLATISVNKQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGSAIFGGEHFMLEETD
WYLLNLFRLWWHYGISFLRLQMWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTRFIDDVVSAVLRASYGQSAAMPAFAGAMSLAGAQQSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVSLVHGYNSSYFGFPDPKLFPFANILTTDFPSFFCTLD
NICPVNISASFRRKQPQEAADVVRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPLYGSRPTL
PRFALHDQLFYLNALEWAASSVEVMVAAKNVALLAYNRWYQDLQKIDQKDLMHKVKTEL

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
237-243, 429-435